RAW SEQUENCE LISTING   DATE: 05/01/2003
PATENT APPLICATION: US/09/687,528   TIME: 13:15:57

Input Set : A:\EP.txt
Output Set: N:\CRF4\05012003\I687528.raw


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 3 <110> APPLICANT: Stern, David M
 4        Schmidt, Anne Marie
 5        Marso, Steven
 6        Topol, Eric
 7        Lincoff, A. Michael
 9 <120> TITLE OF INVENTION: A Method for Inhibiting New Tissue Growth in Blood Vessels
in a Patient
10         Subjected to Blood Vessel Injury
12 <130> FILE REFERENCE: 0575-62096/JPW/AJM/AAB
14 <140> CURRENT APPLICATION NUMBER: 09/687,528
15 <141> CURRENT FILING DATE: 2000-10-13
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 416
23 <212> TYPE: PRT
24 <213> ORGANISM: Cow
26 <400> SEQUENCE: 1
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33              20                  25                  30
36 Pro Leu Val Leu Asn Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
37          35                  40                  45
40 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
41      50                  55                  60
44 Ser Pro Gln Gly Asp Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn
45 65                  70                  75                  80
48 Gly Ser Leu Leu Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Thr Phe
49              85                  90                  95
52 Arg Cys Arg Ala Thr Ser Arg Ser Gly Lys Glu Thr Lys Ser Asn Tyr
53              100                 105                 110
56 Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
57              115                 120                 125
60 Ala Ser Glu Leu Met Ala Gly Val Pro Asn Lys Val Gly Thr Cys Val
61      130                 135                 140
64 Ser Glu Gly Gly Tyr Pro Ala Gly Thr Leu Asn Trp Leu Leu Asp Gly
65 145                 150                 155                 160
68 Lys Thr Leu Ile Pro Asp Gly Lys Gly Val Ser Val Lys Glu Glu Thr
69              165                 170                 175
72 Lys Arg His Pro Lys Thr Gly Leu Phe Thr Leu His Ser Glu Leu Met
73              180                 185                 190
76 Val Thr Pro Ala Arg Gly Gly Ala Leu His Pro Thr Phe Ser Cys Ser
77          195                 200                 205
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 80 Phe Thr Pro Gly Leu Pro Arg Arg Arg Ala Leu His Thr Ala Pro Ile
 81     210                 215                 220
 84 Gln Leu Arg Val Trp Ser Glu His Arg Gly Gly Glu Gly Pro Asn Val
 85 225                 230                 235                 240
 88 Asp Ala Val Pro Leu Lys Glu Val Gln Leu Val Val Glu Pro Glu Gly
 89                 245                 250                 255
 92 Gly Ala Val Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Ala Pro
 93                 260                 265                 270
 96 Ala Gln Pro Pro Pro Gln Ile His Trp Ile Lys Asp Gly Arg Pro Leu
 97             275                 280                 285
100 Pro Leu Pro Pro Gly Pro Met Leu Leu Leu Pro Glu Val Gly Pro Glu
101         290                 295                 300
104 Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr His Pro Ser His Gly Pro
105 305                 310                 315                 320
108 Gln Glu Ser Arg Ala Val Ser Val Thr Ile Ile Glu Thr Gly Glu Glu
109                 325                 330                 335
112 Gly Thr Thr Ala Gly Ser Val Glu Gly Pro Gly Leu Glu Thr Leu Ala
113             340                 345                 350
116 Leu Thr Leu Gly Ile Leu Gly Gly Leu Gly Thr Val Ala Leu Leu Ile
117         355                 360                 365
120 Gly Val Ile Val Trp His Arg Arg Arg Gln Arg Lys Gly Gln Glu Arg
121     370                 375                 380
124 Lys Val Pro Glu Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu
125 385                 390                 395                 400
128 Asn Gln Pro Glu Glu Pro Glu Ala Ala Glu Ser Ser Thr Gly Gly Pro
129             405                 410                 415
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133 <211> LENGTH: 1426
134 <212> TYPE: DNA
135 <213> ORGANISM: Cow
137 <400> SEQUENCE: 2
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140 gggacagtca cggggggacca aaacatcaca gcccggatcg ggaagccact ggtgctgaac   120
142 tgcaagggag cccccaagaa accaccccag cagctggaat ggaaactgaa cacaggccgg   180
144 acagaagctt ggaaagtcct gtctccccag ggagacccct gggatagcgt ggctcgggtc   240
146 ctccccaacg gctccctcct cctgccggct gttgggatcc aggatgaggg gactttccgg   300
148 tgccgggcaa cgagccggag cggaaaggag accaagtcta actaccgagt ccgagtctat   360
150 cagattcctg ggaagccaga aattgttgat cctgcctctg aactcatggc tggtgtcccc   420
152 aataaggtgg ggacatgtgt gtccgagggg ggctaccctg cagggactct taactggctc   480
154 ttggatggga aaactctgat tcctgatggc aaaggagtgt cagtgaagga agagaccaag   540
156 agacacccaa agacagggct tttcacgctc cattcggagc tgatggtgac cccagctcgg   600
158 ggaggagctc tccacccccac cttctcctgt agcttcaccc ctggccttcc ccggcgccga   660
160 gccctgcaca cggccccccat ccagctcagg gtctggagtg agcaccgagg tggggagggc   720
162 cccaacgtgg acgctgtgcc actgaaggaa gtccagttgg tggtagagcc agaagggggga   780
164 gcagtagctc ctggtggtac tgtgaccttg acctgtgaag ccccgccca gcccccacct    840
166 caaatccact ggatcaagga tggcaggccc ctgcccttc cccctggccc catgctgctc   900
168 ctcccagagg tagggcctga ggaccaggga acctacagtt gtgtggccac ccatcccagc   960
170 catgggcccc aggagagccg tgctgtcagc gtcacgatca tcgaaacagg cgaggagggg  1020
172 acgactgcag gctctgtgga agggccgggg ctggaaaccc tagccctgac cctggggatc  1080
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174 ctgggaggcc tggggacagt cgccctgctc attggggtca tcgtgtggca tcgaaggcgg    1140
176 caacgcaaag gacaggagag gaaggtcccg gaaaaccagg aggaggaaga ggaggagaga    1200
178 gcggaactga accagccaga ggagcccgag gcggcagaga gcagcacagg agggccttga    1260
180 ggagcccacg gccagacccg atccatcagc cccttttctt ttcccacact ctgttctggc    1320
182 cccagaccag ttctcctctg tataatctcc agcccacatc tcccaaactt tcttccacaa    1380
184 ccagagcctc ccacaaaaag tgatgagtaa acacctgcca cattta                   1426
```

187 <210> SEQ ID NO: 3
188 <211> LENGTH: 404
189 <212> TYPE: PRT
190 <213> ORGANISM: Human
192 <400> SEQUENCE: 3

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195 1               5                   10                  15
198 Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
199             20                  25                  30
202 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
203         35                  40                  45
206 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
207     50                  55                  60
210 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
211 65                  70                  75                  80
214 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
215                 85                  90                  95
218 Phe Arg Cys Arg Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
219             100                 105                 110
222 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
223         115                 120                 125
226 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
227     130                 135                 140
230 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
231 145                 150                 155                 160
234 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
235                 165                 170                 175
238 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
239             180                 185                 190
242 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
243         195                 200                 205
246 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
247     210                 215                 220
250 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
251 225                 230                 235                 240
254 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
255                 245                 250                 255
258 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
259             260                 265                 270
262 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
263         275                 280                 285
266 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
267         290                 295                 300
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```
270 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
271 305             310             315                 320
274 Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
275             325             330             335
278 Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly
279             340             345             350
282 Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
283         355             360             365
286 Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu
287     370             375             380
290 Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
291 385             390             395             400
294 Thr Gly Gly Pro
298 <210> SEQ ID NO: 4
299 <211> LENGTH: 1391
300 <212> TYPE: DNA
301 <213> ORGANISM: Human
303 <400> SEQUENCE: 4
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306 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgtaagggg   120
308 gcccccaaga aaccacccca gcggctggaa tggaaactga acacaggccg gacagaagct   180
310 tggaaggtcc tgtctcccca gggaggaggc ccctgggaca gtgtggctcg tgtccttccc   240
312 aacggctccc tcttccttcc ggctgtcggg atccaggatg aggggatttt ccggtgcagg   300
314 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt   360
316 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tcccaataag   420
318 gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat   480
320 gggaagcccc tggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac   540
322 cctgagacag ggctcttcac actgcagtcg gagctaatgg tgaccccagc ccggggagga   600
324 gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg   660
326 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg   720
328 gtggtggagc cagaaggtgg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa   780
330 gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgcccctt   840
332 cccccccagcc ctgtgctgat cctccctgag atagggcctc aggaccaggg aacctacagc   900
334 tgtgtggcca cccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc   960
336 atcgaaccag gcgaggaggg gccaactgca ggctctgtgg gaggatcagg gctgggaact  1020
338 ctagccctgg ccctggggat cctgggaggc ctggggacag ccgccctgct cattggggtc  1080
340 atcttgtggc aaaggcggca acgccgagga gaggagagga aggccccaga aaaccaggag  1140
342 gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt  1200
344 actggagggc cttgaggggc ccacagacag atcccatcca tcagctccct tttctttttc  1260
346 ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc  1320
348 ccaccttgcc aagctttctt ctacaaccag agccccccac aatgatgatt aaacacctga  1380
350 cacatcttgc a                                                       1391
353 <210> SEQ ID NO: 5
354 <211> LENGTH: 403
355 <212> TYPE: PRT
356 <213> ORGANISM: Mouse
358 <400> SEQUENCE: 5
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361 1             5               10              15
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Output Set: N:\CRF4\05012003\I687528.raw

```
364 Trp Gly Ala Val Ala Gly Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu
365         20                  25                  30
368 Pro Leu Val Leu Ser Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
369         35                  40                  45
372 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
373         50                  55                  60
376 Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn
377 65                  70                  75                  80
380 Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe
381             85                  90                  95
384 Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr
385             100                 105                 110
388 Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
389             115                 120                 125
392 Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val
393         130                 135                 140
396 Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly
397 145                 150                 155                 160
400 Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr
401                 165                 170                 175
404 Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr
405             180                 185                 190
408 Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser
409         195                 200                 205
412 Phe Ser Leu Gly Leu Pro Arg Arg Arg Pro Leu Asn Thr Ala Pro Ile
413         210                 215                 220
416 Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu
417 225                 230                 235                 240
420 Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu
421                 245                 250                 255
424 Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
425             260                 265                 270
428 Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro
429             275                 280                 285
432 Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His
433         290                 295                 300
436 Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr
437 305                 310                 315                 320
440 Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly
441             325                 330                 335
444 Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly Val
445             340                 345                 350
448 Val Ala Leu Leu Val Gly Ala Ile Leu Trp Arg Lys Arg Gln Pro Arg
449             355                 360                 365
452 Arg Glu Glu Arg Lys Ala Pro Glu Ser Gln Glu Asp Glu Glu Glu Arg
453         370                 375                 380
456 Ala Glu Leu Asn Gln Ser Glu Glu Ala Glu Met Pro Glu Asn Gly Ala
457 385                 390                 395                 400
460 Gly Gly Pro
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/687,528

DATE: 05/01/2003
TIME: 13:15:58

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